

Figure 1 (SEQ ID NO:724)

85P1B3 SSH sequence and GenBank homology to OIP5

GATCAGAGGACACATGGGACTCTGCATCTTAATTCTAAATITACAGTCAAAGACATTTCAAGAGATAAGTATTATGAATTCAATAAGAATCTAAAGTAAGTCTTAAGGCAAATAGCTATAAAA
GAGAAGAACCTTCTAGTCTCATCTTCTAAAAAACAGCTTCAACAAATAATTGGAAAATCAGCTAAAGGTAAATAGAAACTGCATTCCCCTCCATTCTGAAGGCCAATCTTTCAAGAAATGACTAACGAGCACCTGTTGAAGACAGCAATAAGCCTGAACCTGACACTCAAGCTTGGTACAGGATC

gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein... 632 e-179
gb|AF158642.1|AF158642 Homo sapiens metalloproteinase-disin... 42 0.12
gb|AC005075.2|AC005075 Homo sapiens clone RG219E16, complet... 42 0.12
emb|AL096773.6|HS1000E10 Human DNA sequence from clone 1000... 40 0.48

>gb|AF025441.1|AF025441 Homo sapiens Opa-interacting protein OIP5 mRNA, partial cds
Length = 1197

Score = 632 bits (319), Expect = e-179

Identities = 319/319 (100%)

Strand = Plus / Minus

Query: 1 gatcagaggacacatggactctgcatcttaattcctaaatttacagtcaaagacat 60
||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 1013 gatcagaggacacatggactctgcatcttaattcctaaatttacagtcaaagacat 954

Query: 61 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaatacgta 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 953 cagagataagtattatgaattcaataagaatctaaagtaagttcttaaggcaaatacgta 894

Query: 121 taaaagagaagaatccttagtctctatcttctaaaaacagcttcacaaataattggaa 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 893 taaaagagaagaatccttagtctctatcttctaaaaacagcttcacaaataattggaa 834

Query: 181 aatcagcctaaaggtaaatagaaactgcatttccccccattcttgaagccaatctttt 240
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 833 aatcagcctaaaggtaaatagaaactgcatttccccccattcttgaagccaatctttt 774

Query: 241 caagaatgactaaggcacctgttgaagacagcaataaagcctgaacctgacact 300
|||||||
Sbjct: 773 caagaatgactaaggcacctgttgaagacagcaataaagcctgaacctgacact 714

Figure 2

cDNA Sequence and ORF of 85P1B3/OIPS clone A
(SEQ ID NO:727)

5' ↓ 9 18 27 36 45 54
 5' GGC TGC GGG AAG ATG GCG GCT CAG CCG CTG CGG CAT CGC TCA CGT TGT GCA ACG
 (SEQ ID NO:728) → M A A Q P L R H R S R C A T
 63 72 81 90 99 108
 CCG CCC CGG GGG GAC TTT TGT GGT GGC ACT GAG AGG GCG ATT GAC CAA GCT TCT
 P P R G D F C G G T E R A I D Q A S
 117 126 135 144 153 162
 TTT ACG ACC TCC ATG GAG TGG GAT ACG CAG GTG GTG AAG GGG TCC TCG CCG CTC
 F T T S M E W D T Q V V K G S S P L
 171 180 189 198 207 216
 GGC CCC GCA GGG CTG GGG GCT GAG GAG CCA GCC GCC GGC CCG CAG CTG CCG TCT
 G P A G L G A E E P A A G P Q L P S
 225 234 243 252 261 270
 TGG CTG CAG CCT GAG AGG TGC GCT GTG TTC CAG TGC GCA CAG TGT CAC GCA GTG
 W L Q P E R C A V F Q C A Q C H A V
 279 288 297 306 315 324
 CTC GCC GAC TCG GTG CAC CTC GCC TGG GAC CTG TCG CGG TCC CTC GGG GCC GTG
 L A D S V H L A W D L S R S L G A V
 333 342 351 360 369 378
 GTC TTC TCC AGA GTT ACA AAT AAC GTC GTT TTG GAA GCG CCC TTC CTA GTT GGC
 V F S R V T N N V V L E A P F L V G
 387 396 405 414 423 432
 ATT GAA GGT TCA CTC AAA GGC AGT ACT TAC AAC CTT TTA TTC TGT GGT TCT TGT
 I E G S L K G S T Y N L L F C G S C
 441 450 459 468 477 486
 GGG ATT CCC GTT GGT TTC CAT CTG TAT TCT ACC CAT GCT GGC CTG GCT GCC TTG
 G I P V G F H L Y S T H A A L A A L
 495 504 513 522 531 540
 AGA GGT CAC TTC TGC CTT TCC AGT GAC AAA ATG GTG TGC TAT CTC TTA AAA ACA
 R G H F C L S S D K M V C Y L L K T
 549 558 567 576 585 594
 AAA GCC ATA GTC ATT GCA TCA GAG ATG GAT ATT CAA AAT GTT CCT CTA TCA GAA
 K A I V N A S E M D I Q N V P L S E
 603 612 621 630 639 648
 AAG ATT GCA GAG CTG AAA GAG AAG ATA GTG CTA ACG CAC AAT CGC TTA AAA TCA
 K I A E L K E K I V L T H N R L K S

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657	666	675	684	693	702												
CTA ATG AAG ATT CTG AGT GAA GTG ACT CCT GAC CAG TCC AAG CCA GAA AAC TGA																	

L	M	K	I	L	S E V T P D Q S K P E N *												
711				720	729	738	747		756								
TCC	TGT	ACC	AAA	GCT	TGA	GTG	TCA	GGT	TCA	GGC	TTT	ATT	GCT	GTC	TTC	AAC	AAC
-----						-----						-----					
765				774	783	792	801		810								
AGG	TGC	TGC	TTA	GTC	ATT	TCT	TGA	AAA	AGA	TTG	GCT	TCA	AGA	ATG	GAG	GGG	AAA
-----						-----						-----					
819				828	837	846	855		864								
TGC	AGT	TTC	TAT	TTA	CCT	TTA	GGC	TGA	TTT	TCC	AAA	TTA	TTT	GTG	AAG	CTG	TTT
-----						-----						-----					
873				882	891	900	909		918								
TTA	GAA	GAT	GAG	AGA	CTA	AGG	ATT	CTT	CTC	TTT	TAT	AGC	TAT	TTG	CCT	TAA	GAA
-----						-----						-----					
927				936	945	954	963		972								
CTT	ACT	TTA	GAT	TCT	TAT	TGA	ATT	CAT	AAT	ACT	TAT	CTC	TGA	AAA	TGT	CTT	TGA
-----						-----						-----					
981				990	999	1008	1017		1026								
CTG	TAA	ATT	TAG	GAA	TTA	AGA	TGC	AGA	GTC	CCA	TGT	GTC	CTC	TGA	TCT	AAA	GTT
-----						-----						-----					
1035				1044	1053	1062	1071		1080								
GCA	TGG	TTG	GTC	TGA	AAA	TAG	AGT	TGG	GCT	TAA	TGT	TGA	CTT	CTA	TTA	CTC	CTG
-----						-----						-----					
1089				1098	1107	1116	1125		1134								
CAT	GGA	GCA	GTT	GTT	ATG	AAT	ACT	AAT	ACA	TCA	CTT	TTT	AAC	TTC	TGT	AAA	ATA
-----						-----						-----					
1143				1152	1161	1170	1179		1188								
CAG	ATC	ATC	ATA	TTC	TAT	AGG	TAA	TGT	TTA	ATA	AAT	TGC	CTG	AAT	AAT	AAA	AAA
-----						-----						-----					
1197				1206	1215	1224	1233		1242								
AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA
-----						-----						-----					
1251				1260													
AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AA 3'
-----						-----						-----					

Figure 3

85P1B3/OIP5 protein sequence. (SEQ ID NO:729)

1 MAAQPLRHRs RCATPPRGDF CGGTERAIDQ ASFTTSMEDW TQVVKGSSPL GPAGLGAEFP
61 AAGPQLPSWL QPERCAVFQG AQCHAVLADS VHLAWDLSRS LGAVVFSRVT NNVVLEAPFL
121 VGIEGSLKGS TYNLLFCGSC GIPVGFHILYS THAALAALRG HFCLSSDKMV CYLLKTKAIV
181 NASEMDIQNV PLSEKIAELK EKIVLTHNRL KSLMKILSEV TPDQSKPEN*

Figure 4

Alignment of 85P1B3 with OIP5.

>gi|2815610|gb|AAC39561.1| (AF025441) Opa-interacting protein OIP5 [Homo sapiens]
Length = 231

Score = 462 bits (1189), Expect = e-130

Identities = 229/229 (100%), Positives = 229/229 (100%)

85P1B3: 1	MAAQPLRHSRCATPPRGDFCGGTERAIDQASFTTSM	MEWDTQVVKGSSPLGPAGLGAEEP	60		
	MAAQPLRHSRCATPPRGDFCGGTERAIDQASFTTSM	MEWDTQVVKGSSPLGPAGLGAEEP			
OIP5: 3	MAAQPLRHSRCATPPRGDFCGGTERAIDQASFTTSM	MEWDTQVVKGSSPLGPAGLGAEEP	62		
85P1B3: 61	AAGPQLPSWLQPERCAVFQCAQCHA	VLDHSVHLAWDLSRS	LGAVVFSRV	TNNVLEAPFL	120
	AAGPQLPSWLQPERCAVFQCAQCHA	VLDHSVHLAWDLSRS	LGAVVFSRV	TNNVLEAPFL	
OIP5: 63	AAGPQLPSWLQPERCAVFQCAQCHA	VLDHSVHLAWDLSRS	LGAVVFSRV	TNNVLEAPFL	122
85P1B3: 121	VGIEGSLKGSTYNNLFCGSCGIPVGFHLYST	HAALAALRGHFC	LSSDKMVCYLLK	TKAIV	180
	VGIEGSLKGSTYNNLFCGSCGIPVGFHLYST	HAALAALRGHFC	LSSDKMVCYLLK	TKAIV	
OIP5: 123	VGIEGSLKGSTYNNLFCGSCGIPVGFHLYST	HAALAALRGHFC	LSSDKMVCYLLK	TKAIV	182
85P1B3: 181	NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLM	KILSEVTPDQSKPEN	229 (SEQ ID NO:730)		
	NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLM	KILSEVTPDQSKPEN			
OIP5: 183	NASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLM	KILSEVTPDQSKPEN	231 (SEQ ID NO:731)		

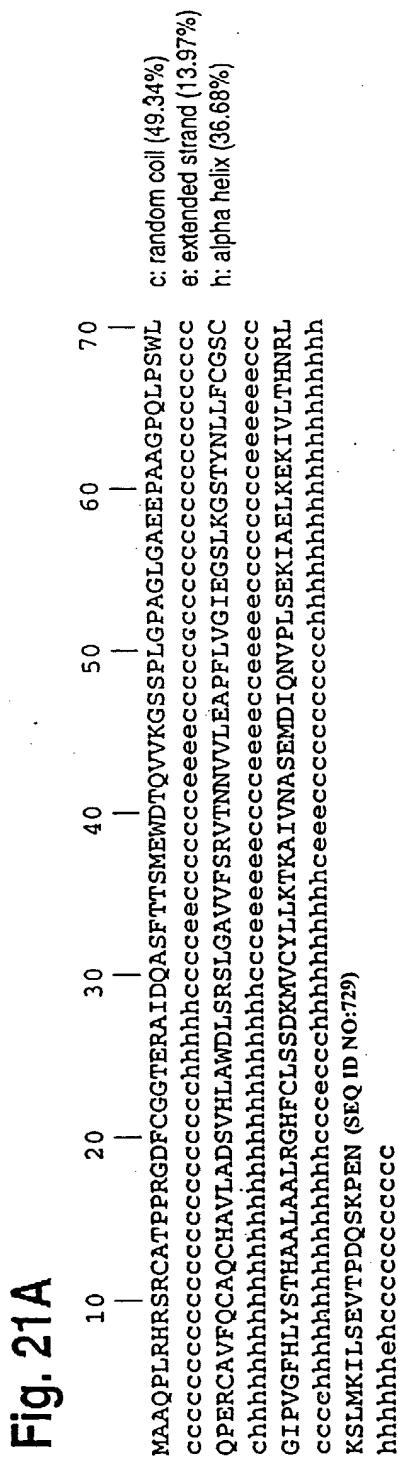


Fig. 21A

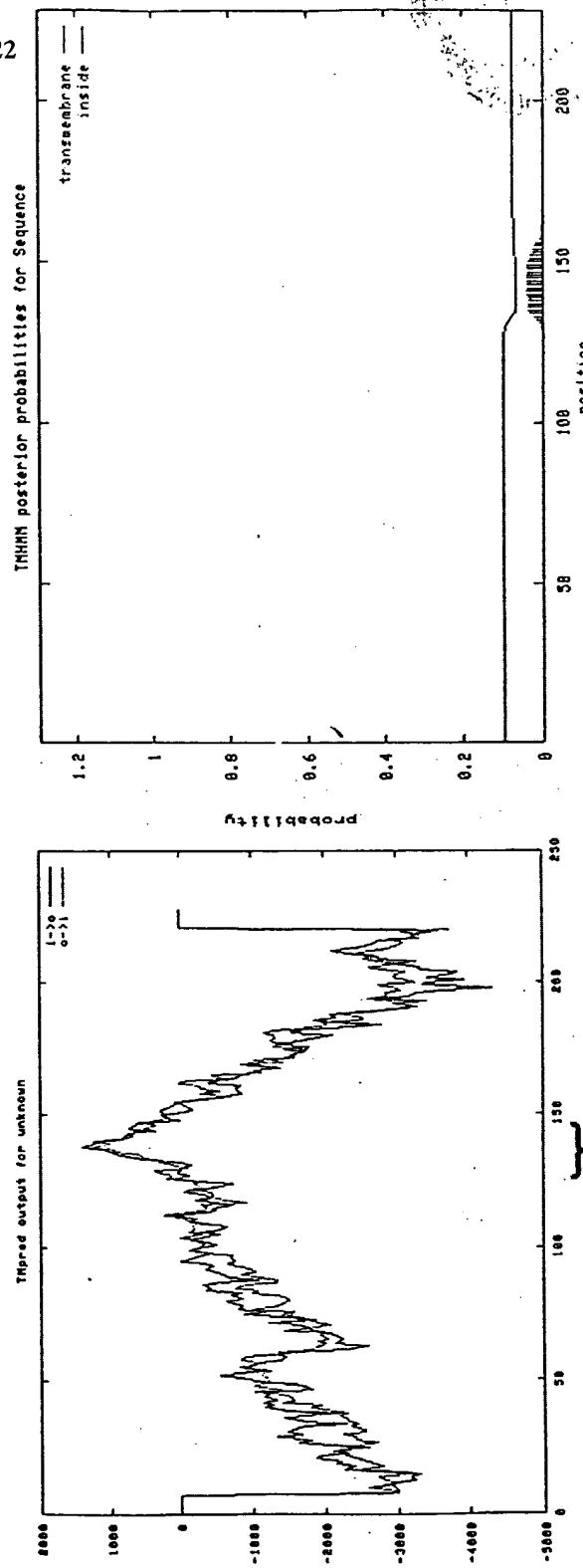


Fig. 21B

1 transmembrane from amino acids 129-149